

SEQUENCE LISTING

<110> Walke, D. Wade
Scoville, John
Donoho, Gregory
Turner, C. Alexander Jr.

<120> Novel Human Proteins and Polynucleotides Encoding the Same

<130> LEX-0180-USA

<150> US 60/206,414

<151> 2000-05-23

<160> 9

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<210> 1

<211> 765

<212> DNA

<213> homo sapiens

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cagtcctgtg	ccgtttcggg	ggtgctgaat	gttacttttc	ctcctctcct	aagtggaaac	360
gacttcctaaa	cagttgagga	aggcagtaat	gtgaagtggg	tttgcaatgt	gaaagccaac	420
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caccaaattcc	aacagacaag	tgagtctttt	cagctgtcaa	tcaccaaagt	cgagaagcct	540
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cacctgattg	ttaaagataa	aactgtgggt	gtaccaatag	agcccattat	tgctgcatgt	660
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<211> 254

<212> PRT

<213> homo sapiens

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65			70				75							80	
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Val Ser Ser Ile Ser Glu Asn Asp Asn Gly Ile Ser Phe Thr Cys Arg
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Leu Gly Arg Asp Gln Ser Val Ser Val Ser Val Val Leu Asn Val Thr
100 105 110
Phe Pro Pro Leu Leu Ser Gly Asn Asp Phe Gln Thr Val Glu Glu Gly
115 120 125
Ser Asn Val Lys Leu Val Cys Asn Val Lys Ala Asn Pro Gln Ala Gln
130 135 140
Met Met Trp Tyr Lys Asn Ser Ser Leu Leu Asp Leu Glu Lys Ser Arg
145 150 155 160
His Gln Ile Gln Gln Thr Ser Glu Ser Phe Gln Leu Ser Ile Thr Lys
165 170 175
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180 185 190
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Glu Gly
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Gln Ala Ser Leu Ile Cys Ala Val Gln Asn His Thr Arg Glu Glu Glu
50 55 60
Leu Leu Trp Tyr Arg Glu Glu Gly Arg Val Asp Leu Lys Ser Gly Asn
65 70 75 80

Lys Ile Asn Ser Ser Ser Val Cys Val Ser Ser Ile Ser Glu Asn Asp
 85 90 95
 Asn Gly Ile Ser Phe Thr Cys Arg Leu Gly Arg Asp Gln Ser Val Ser
 100 105 110
 Val Ser Val Val Leu Asn Val Thr Phe Pro Pro Leu Leu Ser Gly Asn
 115 120 125
 Asp Phe Gln Thr Val Glu Glu Gly Ser Asn Val Lys Leu Val Cys Asn
 130 135 140
 Val Lys Ala Asn Pro Gln Ala Gln Met Met Trp Tyr Lys Asn Ser Ser
 145 150 155 160
 Leu Leu Asp Leu Glu Lys Ser Arg His Gln Ile Gln Gln Thr Ser Glu
 165 170 175
 Ser Phe Gln Leu Ser Ile Thr Lys Val Glu Lys Pro Asp Asn Gly Thr
 180 185 190
 Tyr Ser Cys Ile Ala Lys Ser Ser Leu Lys Thr Glu Ser Leu Asp Phe
 195 200 205
 His Leu Ile Val Lys Asp Lys Thr Val Gly Val Pro Ile Glu Pro Ile
 210 215 220
 Ile Ala Ala Cys Val Val Ile Phe Leu Thr Leu Cys Phe Gly Leu Ile
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 agagaggaag aactgctctg gtaccgagag gaggggagag tggatttgaa atctgsaaac 240
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 ctctcgatt tagagaaaag ccgtcaccaa atccaacaga caagtgagtc ttttcagctg 540
 tcaatcacca aagtcgagaa gcctgacaac ggaacctaca gttgtattgc aaagtcattc 600
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 35 40 45
 Gln Ala Ser Leu Ile Cys Ala Val Gln Asn His Thr Arg Glu Glu Glu

50 55 60
 Leu Leu Trp Tyr Arg Glu Glu Gly Arg Val Asp Leu Lys Ser Gly Asn
 65 70 75 80
 Lys Ile Asn Ser Ser Val Cys Val Ser Ser Ile Ser Glu Asn Asp
 85 90 95
 Asn Gly Ile Ser Phe Thr Cys Arg Leu Gly Arg Asp Gln Ser Val Ser
 100 105 110
 Val Ser Val Val Leu Asn Val Thr Phe Pro Pro Leu Leu Ser Gly Asn
 115 120 125
 Asp Phe Gln Thr Val Glu Glu Gly Ser Asn Val Lys Leu Val Cys Asn
 130 135 140
 Val Lys Ala Asn Pro Gln Ala Gln Met Met Trp Tyr Lys Asn Ser Ser
 145 150 155 160
 Leu Leu Asp Leu Glu Lys Ser Arg His Gln Ile Gln Gln Thr Ser Glu
 165 170 175
 Ser Phe Gln Leu Ser Ile Thr Lys Val Glu Lys Pro Asp Asn Gly Thr
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